What is claimed is:

1. A method for identifying bioactivities or biomolecules using high throughput screening of nucleic acid comprising:

   a) providing a gene library containing a plurality of clones, wherein the DNA for generating the library is obtained from more than one organism;

   b) encapsulating a bioactive substrate and at least one clone of the library in a gel microdroplet, wherein a bioactivity or biomolecule produced by the clone is detectable by a difference in the substrate prior to contacting with the at least one clone as compared to after contacting;

   c) screening the microdroplet with an assay or an analyzer that detects a bioactivity or biomolecule; and

   d) identifying clones detected as positive for a change in the substrate, wherein a change in the substrate is indicative of DNA that encodes a bioactivity or biomolecule.

2. The method of claim 1, wherein the bioactivity is provided by an enzyme is selected from the group consisting of lipases, esterases, proteases, glycosidases, glycosyl transferases, phosphatases, kinases, mono- and dioxygenases, haloperoxidases, lignin peroxidases, diarylpropane peroxidases, epozide hydrolases, nitrile hydratases, nitrilases, transaminases, amidases, and acylases.

3. The method of claim 1, wherein the library is generated in a prokaryotic cell.

4. The method of claim 1, wherein the library is generated in a *Streptomyces* sp.

5. The method of claim 4, wherein the *Streptomyces* is *Streptomyces venezuelae*.

6. The method of claim 3, wherein the prokaryotic cell is gram negative.

7. The method of claim 1, wherein the gene library is an expression library.

8. The method of claim 5, wherein the expression library contains DNA obtained from extremophiles.

9. The method of claim 8, wherein the extremophiles are thermophiles.

10. The method of claim 9, wherein the extremeophiles are selected from the group consisting of hyperthermophiles, psychrophiles, halophiles, psychrotrophs, alkalophiles, and acidophiles.

11. The method of claim 1, wherein the bioactive substrate comprises C12FDG.

12. The method of claim 1, wherein the bioactive substrate comprises a lipophilic tail.

13. The method of claim 1, wherein the the samples are heated before step b).

14. The method of claim 13, wherein the heating is at about 70°C.

15. The method of claim 14, wherein the heating occurs at about 30 minutes.

16. The method of claim 1, wherein the analyzer comprises a fluorescent analyzer.

17. The method of claim 16, wherein the fluorescent analyzer is a FACS apparatus.

18. The method of claim 1, wherein the library is biopanned before step b).

19. The method of claim 4, wherein the prokaryotic cell is *E. coli*.

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20. The method of claim 19, wherein prior to step b), the *E. coli* is transferred to a *Streptomyces* sp.

21. The method of claim 20, wherein the *Streptomyces* sp. is *Streptomyces venezuelae.*

22. The method of claim 1, wherein the library is normalized before step b).

23. The method of claim 1, further comprising co-encapsulating an indicator cell in step b).

24. The method of claim 1, wherein the analyzer is a chromogenic analyzer.

25. The method of claim 1, wherein the assay is an immunoassay.

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26. A method for identifying bioactivities or biomolecules using high throughput screening of nucleic acid comprising:

a) providing a gene library containing a plurality of clones, wherein the nucleic acid for generating the library is obtained from more than one organism;

b) inserting a bioactive substrate into the clones of the library, wherein a change in the substrate is detectable in the presence of a bioactivity or biomolecule;

c) screening the clones with an assay or an analyzer that detects the presence of a bioactivity or a biomolecule; and

d) identifying clones detected as positive for a change in the substrate, wherein a change in the substrate is indicative of DNA that encodes a bioactivity or biomolecule.

27. The method of claim 26, further comprising encapsulation the clone and the bioactive substrate prior to screening.

28. The method of claim 27, wherein the bioactivity is provided by an enzyme is selected from the group consisting of lipases, esterases, proteases, glycosidases, glycosyl transferases, phosphatases, kinases, mono- and dioxygenases, haloperoxidases, lignin peroxidases, diarylpropane peroxidases, epozide hydrolases, nitrile hydratases, nitrilases, transaminases, amidases, and acylases.

29. The method of claim 27, wherein the library is generated in a prokaryotic cell.

30. The method of claim 27, wherein the library is generated in a *Streptomyces* sp.

31. The method of claim 30, wherein the *Streptomyces* is *Streptomyces venezuelae*.

32. The method of claim 29, wherein the prokaryotic cell is gram negative.

33. The method of claim 27, wherein the gene library is an expression library.

34. The method of claim 31, wherein the expression library contains DNA obtained from extremophiles.

35. The method of claim 34, wherein the extremophiles are thermophiles.

36. The method of claim 35, wherein the extremeophiles are selected from the group consisting of hyperthermophiles, psychrophiles, halophiles, psychrotrophs, alkalophiles, and acidophiles.

37. The method of claim 27, wherein the bioactive substrate comprises C12FDG.

38. The method of claim 27, wherein the bioactive substrate comprises a lipophilic tail.

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39. The method of claim 27, wherein the the samples are heated before step b).

40. The method of claim 39, wherein the heating is at about 70°C.

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41. The method of claim 40, wherein the heating occurs at about 30 minutes.

42. The method of claim 27, wherein the analyzer comprises a fluorescent analyzer.

43. The method of claim 42, wherein the fluorescent analyzer is a FACS apparatus.

44. The method of claim 27, wherein the library is biopanned before step b).

45. The method of claim 29, wherein the prokaryotic cell is *E. coli*.

46. The method of claim 45, wherein prior to step b), the *E. coli* is transferred to a myceliate bacteria or fungi.

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47. The method of claim 46, wherein the myceliate fungi is an *Actinomyces* sp.

48. The method of claim 46, wherein the myceliate bacteria is a *Streptomyces* sp.

49. The method of claim 47, wherein the *Streptomyces* sp. is *Streptomyces venezuelae.*

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50. The method of claim 27, wherein the library is normalized before step b).

51. The method of claim 27, further comprising co-encapsulating an indicator cell in step b).

52. The method of claim 27, wherein the analyzer is a chromogenic analyzer.

53. The method of claim 27, wherein the assay is an immunoassay.